



<210> 1

<211> 167

<212> PRT

<213> Homo sapiens

<400> 1

Met Ser Gly Leu Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val  
1 5 10 15

Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr  
20 25 30

Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser  
35 40 45

Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln  
50 55 60

Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly  
65 70 75 80

Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly  
85 90 95

Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr  
100 105 110

Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro



Met Ser Gly Leu Ile Thr Ile Val Val Leu Leu Gly

1

5

10

atc gcc ttt gta gtc tat aag ctg ttc ctg agt gac ggg cag tat tct 277

Ile Ala Phe Val Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Tyr Ser

15

20

25

cct cca ccg tac tct gag tat cct cca ttt tcc cac cgt tac cag aga 325

Pro Pro Pro Tyr Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg

30

35

40

ttc acc aac tca gca gga cct cct ccc cca ggc ttt aag tct gag ttc 373

Phe Thr Asn Ser Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe

45

50

55

60

aca gga cca cag aat act ggc cat ggt gca act tct ggt ttt ggc agt 421

Thr Gly Pro Gln Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser

65

70

75

gct ttt aca gga caa caa gga tat gaa aat tca gga cca ggg ttc tgg 469

Ala Phe Thr Gly Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp

80

85

90

aca ggc ttg gga act ggt gga ata cta gga tat ttg ttt ggc agc aat 517

Thr Gly Leu Gly Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn

95

100

105

aga gcg gca aca ccc ttc tca gac tcg tgg tac tac ccg tcc tat cct 565

Arg Ala Ala Thr Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro



ttttgagctc tgaagctttg aatcattcag tgggtggagat ggccttctgg taactgaata 1254

ttaccttctg taggaaaagg tggaaaataa gcatctagaa ggttggttgat aatgactctg 1314

tgctggcaaa aatgcttgaa acctctatat ttctttcgtt cataagaggt aaaggtcaaa 1374

tttttcaaca aaagtctttt aataacaaaa gcatgcagtt ctctgtgaaa tctcaaatat 1434

tggtgtaata gtctgtttca atcttaaaaa gaatcaat 1472

<210> 3

<211> 339

<212> PRT

<213> Homo sapiens

<400> 3

Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu

1 5 10 15

Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn

20 25 30

Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His

35 40 45

Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu

50 55 60

Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val  
 65 70 75 80

Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu  
 85 90 95

Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val  
 100 105 110

Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly  
 115 120 125

Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln  
 130 135 140

Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp  
 145 150 155 160

Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu  
 165 170 175

Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu  
 180 185 190

Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro  
 195 200 205

Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro  
 7/735

210

215

220

Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His

225

230

235

240

Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr

245

250

255

Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile

260

265

270

Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp

275

280

285

Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn

290

295

300

Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys

305

310

315

320

Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr

325

330

335

Arg Arg Arg

&lt;210&gt; 4

&lt;211&gt; 1924

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (115).. (1131)

<400> 4

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cccaggttcg gcccgtaggc gtctggcagc ccggcgccat cttcatcgag cgcc atg 117

Met

1

gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc 165

Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly

5

10

15

ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac 213

Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp

20

25

30

cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat 261

Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr

35

40

45

gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa 309

Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys

50

55

60

65



acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc 693

Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe

180

185

190

ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca 741

Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro

195

200

205

ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct ccc 789

Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro

210

215

220

225

cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggc cat ggt 837

Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly

230

235

240

gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa 885

Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu

245

250

255

aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta 933

Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu

260

265

270

gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg 981

Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser

275

280

285

tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg 1029



tggtggagat ggccttcttg taactgaata ttaccttctg taggaaaagg tggaaaataa 1721

gcatctagaa ggttggttg aatgactctg tgctggcaaa aatgcttgaa acctctatat 1781

ttctttcgtt cataagaggt aaaggtcaaa tttttcaaca aaagtctttt aataacaaaa 1841

gcatgcagtt ctctgtgaaa tctcaaatat tgttgtaata gtctgtttca atcttaaaaa 1901

gaatcaataa aaacaaacaa ggg 1924

<210> 5

<211> 127

<212> PRT

<213> Homo sapiens

<400> 5

Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile

1 5 10 15

Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly

20 25 30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val

35 40 45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val

50 55 60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala  
 65 70 75 80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile  
 85 90 95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe  
 100 105 110

Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser  
 115 120 125

<210> 6

<211> 702

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (225)..(605)

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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcacct 180



atg gag atg agt cct tgg ttc caa ttc atg ctg ttt atc ctg cag ctg 572

Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu

105

110

115

gac att gcc ttc aag cta aac aac caa atc agt taagtgtact ctcctctcat 625

Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser

120

125

ccctttcttc cctttgagca ttgccctctt tgggttcttt ttgagccaat tctaataaaa 685

gtaaaaatgg taatagt

702

<210> 7

<211> 233

<212> PRT

<213> Homo sapiens

<400> 7

Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile

1

5

10

15

Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly

20

25

30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val

35

40

45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val

50	55	60
Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala		
65	70	75 80
Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile		
	85	90 95
Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe		
	100	105 110
Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu		
	115	120 125
Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala		
	130	135 140
Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu		
145	150	155 160
Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr		
	165	170 175
Tyr Glu Cys Asp Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly		
	180	185 190
Val Val Leu Glu Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser		
	195	200 205

Gly Lys Ser His Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr  
 210 215 220

Pro Ser Gly Met Val Phe His Arg Val  
 225 230

<210> 8

<211> 2409

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225).. (923)

<400> 8

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 ggcgcccttc gtcccgggtcc catcctcgcc gcgctccagc acctctgaag ttttgcagcg 120  
 cccagaaagg aggcgaggaa ggaggggagtg tgtgagagga gggagcaaaa agctcaccct 180  
 aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236  
 Met Ala Gly Ala

1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284  
 Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

5	10	15	20	
ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct				332
Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala				
	25	30	35	
cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat				380
Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp				
	40	45	50	
gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc				428
Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro				
	55	60	65	
aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa				476
Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu				
	70	75	80	
att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac				524
Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His				
	85	90	95	100
atg gag atg agt cct tgg ttc caa ttc atg ctg ttt atc ctg cag ctg				572
Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu				
	105	110	115	
gac att gcc ttc aag cta aac aac caa atc aga gaa aat gca gaa gtc				620
Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val				
	120	125	130	



ggcatcttct atgcgatgct tctgtccttc tggatcatct tctgtggcga gcacatgatg 1023

gatcagcacg agcggaacca catcgcaggg tattggaagc aagtcggacc cattgccgtt 1083

ggctccttct gcctcttcat atttgacatg tgtgagagag gggtacaact cacgaatccc 1143

ttctacagta tctggactac agacattgga acagagctgg ccatggcctt catcatcgtg 1203

gctggaatct gcctctgcct ctacttcctg tttctatgct tcatgggtatt tcaggtgttt 1263

cggaacatca gtgggaagca gtccagcctg ccagctatga gcaaagtccg gcggctacac 1323

tatgaggggc taatTTTTtag gttcaagttc ctcatgctta tcaccttggc ctgcgctgcc 1383

atgactgtca tcttcttcat cgttagtcag gtaacggaag gccattggaa atggggcggc 1443

gtcacagtcc aagtgaacag tgcctttttc acaggcatct atgggatgtg gaatctgtat 1503

gtctttgctc tgatgttctt gtatgcacca tcccataaaa actatggaga agaccagtcc 1563

aatggcgatc tgggtgtcca tagtggggaa gaactccagc tcaccaccac tatcaccat 1623

gtggacggac ccactgagat ctacaagttg acccgcaagg aggcccagga gtaggaggct 1683

gcagcgcccg gctgggacgg tctctccata cccagcccc tctaactaga gtggggagca 1743

tgccagagag agctcaatgt acaaatgaat gcctcatggc tcttagctgt ggtttcttgg 1803

accagcggca tggacatttg tcagtttgcc ttctgacggt agcttttgga ggaagattcc 1863



1	5	10	15
Leu Ser Cys Leu Ala Leu Ser Val Leu Leu Leu Ala Gln Leu Ser Asp			
20	25	30	
Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile Cys Pro Pro			
35	40	45	
Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn Ile Ser Gln Lys			
50	55	60	
Asp Cys Asp Cys Leu His Val Val Glu Pro Met Pro Val Arg Gly Pro			
65	70	75	80
Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu Cys Lys Tyr Glu Glu Arg			
85	90	95	
Ser Ser Val Thr Ile Lys Val Thr Ile Ile Ile Tyr Leu Ser Ile Leu			
100	105	110	
Gly Leu Leu Leu Leu Tyr Met Val Tyr Leu Thr Leu Val Glu Pro Ile			
115	120	125	
Leu Lys Arg Arg Leu Phe Gly His Ala Gln Leu Ile Gln Ser Asp Asp			
130	135	140	
Asp Ile Gly Asp His Gln Pro Phe Ala Asn Ala His Asp Val Leu Ala			
145	150	155	160



ctg ctg gcg cag ctg tca gac gcc gcc aag aat ttc gag gat gtc aga 208

Leu Leu Ala Gln Leu Ser Asp Ala Ala Lys Asn Phe Glu Asp Val Arg

30

35

40

tgt aaa tgt atc tgc cct ccc tat aaa gaa aat tct ggg cat att tat 256

Cys Lys Cys Ile Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr

45

50

55

aat aag aac ata tct cag aaa gat tgt gat tgc ctt cat gtt gtg gag 304

Asn Lys Asn Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu

60

65

70

ccc atg cct gtg cgg ggg cct gat gta gaa gca tac tgt cta cgc tgt 352

Pro Met Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys

75

80

85

gaa tgc aaa tat gaa gaa aga agc tct gtc aca atc aag gtt acc att 400

Glu Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile

90

95

100

105

ata att tat ctc tcc att ttg ggc ctt cta ctt ctg tac atg gta tat 448

Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Leu Tyr Met Val Tyr

110

115

120

ctt act ctg gtt gag ccc ata ctg aag agg cgc ctc ttt gga cat gca 496

Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly His Ala

125

130

135

cag ttg ata cag agt gat gat gat att ggg gat cac cag cct ttt gca 544

Gln Leu Ile Gln Ser Asp Asp Asp Ile Gly Asp His Gln Pro Phe Ala

140

145

150

aat gca cac gat gtg cta gcc cgc tcc cgc agt cga gcc aac gtg ctg 592

Asn Ala His Asp Val Leu Ala Arg Ser Arg Ser Arg Ala Asn Val Leu

155

160

165

aac aag gta gaa tat gca cag cag cgc tgg aag ctt caa gtc caa gag 640

Asn Lys Val Glu Tyr Ala Gln Gln Arg Trp Lys Leu Gln Val Gln Glu

170

175

180

185

cag cga aag tct gtc ttt gac cgg cat gtt gtc ctc agc taattgggaa 689

Gln Arg Lys Ser Val Phe Asp Arg His Val Val Leu Ser

190

195

ttgaattcaa ggtgactaga aagaaacagg cagacaactg gaaagaactg actgggtttt 749

gctgggttttc attttaatac cttgttgatt tcaccaactg ttgctggaag attcaaaaact 809

ggaagcaaaa acttgcttga tttttttttc ttgttaacgt aataatagag acatttttta 869

aagcacacag ctcaaagtca gccataagt cttttcctat ttgtgacttt tactaataaa 929

aataaatctg cctgtaaatt atcttgaagt cctttacctg gaacaagcac tctctttttc 989

accacatagt tttaacttga ctttcaagat aattttcagg gtttttgttg ttgttggttt 1049

ttgtttgttt gttttggtgg gagaggggag ggatgcctgg gaagtgggta acaacttttt 1109



35	40	45
Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe Pro Lys Pro		
50	55	60
Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp Glu Ala Glu		
65	70	75 80
Arg Thr Lys Ala Glu Ala Thr Ile Pro Leu Val Pro Gly Arg Asp Glu		
85	90	95
Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln Leu Arg Ile		
100	105	110
Gly Asn Asp Gly Ile Phe Met Leu Thr Phe Phe Met Ala Phe Leu Phe		
115	120	125
Asn Trp Ile Gly Phe Phe Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala		
130	135	140
Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp		
145	150	155 160
Ile Leu Ile Val Arg Phe Ser Thr Tyr Phe Pro Gly Tyr Phe Asp Gly		
165	170	175
Gln Tyr Trp Leu Trp Trp Val Phe Leu Val Leu Gly Phe Leu Leu Phe		
180	185	190

Leu Arg Gly Phe Ile Asn Tyr Ala Lys Val Arg Lys Met Pro Glu Thr

195

200

205

Phe Ser Asn Leu Pro Arg Thr Arg Val Leu Phe Ile Tyr

210

215

220

<210> 12

<211> 1864

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (153)..(815)

<400> 12

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cccctcggcc tcccagcgct cccaagccgc agcggccgcg ccccttcagc tagctcgctc 120

gctcgctctg cttccctgct gccggctgcg cc atg gcg ttg gcg ttg gcg gcg 173

Met Ala Leu Ala Leu Ala Ala

1

5

ctg gcg gcg gtc gag ccg gcc tgc ggc agc cgg tac cag cag ttg cag 221

Leu Ala Ala Val Glu Pro Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln

10

15

20

aat gaa gaa gag tct gga gaa cct gaa cag gct gca ggt gat gct cct 269

Asn Glu Glu Glu Ser Gly Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro

25

30

35

cca cct tac agc agc att tct gca gag agc gca gca tat ttt gac tac 317

Pro Pro Tyr Ser Ser Ile Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr

40

45

50

55

aag gat gag tct ggg ttt cca aag ccc cca tct tac aat gta gct aca 365

Lys Asp Glu Ser Gly Phe Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr

60

65

70

aca ctg ccc agt tat gat gaa gcg gag agg acc aag gct gaa gct act 413

Thr Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr

75

80

85

atc cct ttg gtt cct ggg aga gat gag gat ttt gtg ggt cgg gat gat 461

Ile Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp

90

95

100

ttt gat gat gct gac cag ctg agg ata gga aat gat ggg att ttc atg 509

Phe Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met

105

110

115

tta act ttt ttc atg gca ttc ctc ttt aac tgg att ggg ttt ttc ctg 557

Leu Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu

120

125

130

135

tct ttt tgc ctg acc act tca gct gca gga agg tat ggg gcc att tca 605

Ser Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser  
 140 145 150

gga ttt ggt ctc tct cta att aaa tgg atc ctg att gtc agg ttt tcc 653  
 Gly Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser  
 155 160 165

acc tat ttc cct gga tat ttt gat ggt cag tac tgg ctc tgg tgg gtg 701  
 Thr Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val  
 170 175 180

ttc ctt gtt tta ggc ttt ctc ctg ttt ctc aga gga ttt atc aat tat 749  
 Phe Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr  
 185 190 195

gca aaa gtt cgg aag atg cca gaa act ttc tca aat ctc ccc agg acc 797  
 Ala Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr  
 200 205 210 215

aga gtt ctc ttt att tat taaagatggt ttctggcaaa ggccttcctg 845  
 Arg Val Leu Phe Ile Tyr  
 220

catttatgaa ttctctctca agaagcaaga gaacacctgc aggaagtga tcaagatgca 905

gaacacagag gaataatcac ctgctttaa aaaataaagt actgttgaaa agatcatttc 965

tctctatattg ttcttaggtg taaaatttta atagttaatg cagaattctg taatcattga 1025



<210> 13

<211> 242

<212> PRT

<213> Homo sapiens

<400> 13

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn

1 5 10 15

Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser

20 25 30

Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu

35 40 45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val

50 55 60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro

65 70 75 80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu

85 90 95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln

100 105 110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala

115 120 125



<213> Homo sapiens

<220>

<221> CDS

<222> (13).. (738)

<400> 14

gagccgggca gg atg gat cac cac cag ccg ggg act ggg cgc tac cag gtg 51

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val

1

5

10

ctt ctt aat gaa gag gat aac tca gaa tca tcg gct ata gag cag cca 99

Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro

15

20

25

cct act tca aac cca gca ccg cag att gtg cag gct gcg tct tca gca 147

Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala

30

35

40

45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195

Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr

50

55

60

gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat 243

Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr

65

70

75

ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat 291

Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp

80

85

90

gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa 339

Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu

95

100

105

aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc 387

Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe

110

115

120

125

agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg 435

Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu

130

135

140

gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc 483

Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser

145

150

155

ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga 531

Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly

160

165

170

ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat 579

Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp

175

180

185

tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt 627

Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe

190

195

200

205

ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta 675

Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu

210

215

220

aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg 723

Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg

225

230

235

tat ttc ttc tta ttg tagagactgc atcaaccga cattccttcc ttataccaat 778

Tyr Phe Phe Leu Leu

240

gtgaaatttc cagatcatct gtaaacctac aactttaata gaagactact aataacagaa 838

gacaaattag tgaagaaaag acggagtttc gaaattgaat ggcagggtgg tttttgctta 898

caagccattt ctgttcattc ttttaagtatc tatatttcat ttgttttgca catatgcata 958

tgtgcccatt taagatattt gcatatactt gatagaaacc ataaagttgt agcagttaag 1018

tccagtcaca tttggttaat cagtgtttga tataattgaa agagttgagt ggataaacag 1078

tcttccagct tgtaaatgcc attgacttct gacctgacat ttagtataat aaaaatgaaa 1138

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cttattttatt attagacatt actactaaaa ggtacatcta actattcagg gacatttttc 2218

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<210> 15

<211> 242

<212> PRT

<213> Homo sapiens

<400> 15

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn

1 5 10 15

Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser

20 25 30

Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu

35 40 45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val

50 55 60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro

65 70 75 80







ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat 579

Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp

175

180

185

tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt 627

Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe

190

195

200

205

ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta 675

Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu

210

215

220

aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg 723

Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg

225

230

235

tat ttc ttc tta ttg tagagactgc atcaaccga cattccttcc ttataccaat 778

Tyr Phe Phe Leu Leu

240

gtgaaatttc cagatcatct gtaaaccctac aactttaata gaagactact aataacagaa 838

gacaaattag tgaagaaaag acggagtttc gaaattgaat ggcagggtgg tttttgctta 898

caagccattt ctgttcattc tttaagtatc tatatttcat ttgttttgca catatgcata 958

tgtgcccatt taagatatatt gcatatactt gatagaaacc ataaagttgt agcagttaag 1018

tccagtcaca tttggttaat cagtgtttga tataattgaa agagttgagt ggataaacag 1078

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atttgtcaga tttttgaaca tgatatttac attattattht aggaaaactc ttcctgtaaa 1318

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ggacatacta gtttttaggga ttttcagatg ggaagctgca tttttaggat tgcccatctt 1618

aagagatctt gcaggaagag attgtattag atattatatt tatttcattt aagataattt 1678

tcaaagttaa ttttctaaat aagataattc tcatttgtht ttgtctthta aaaggccaat 1738

aaaatatctt tcagtatcat tgtaataatt ttttagagtht taatttgtaa agcttagcaa 1798

ataaaatctt gtactatgaa tagcttcttg ctttatgact ttaggattaa cttgtaaaaa 1858

acatatcctg aactgagata tgcaaaatac tcattthtcaa gttatggaaa tgtgtthttht 1918



35	40	45
Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro		
50	55	60
Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly		
65	70	75 80
Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp		
85	90	95
His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu		
100	105	110
Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro		
115	120	125
Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr		
130	135	140
Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr		
145	150	155 160
Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro		
165	170	175
Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala		
180	185	190



&lt;211&gt; 2636

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (53)..(1060)

&lt;400&gt; 18

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Met Ala

1

cgc cgg cgg agc cag cga gtc tgc gcg agc ggt ccg agc atg ctc aat 106

Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn

5

10

15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154

Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala

20

25

30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202

Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro

35

40

45

50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250

Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala

55

60

65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac 298  
 Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp  
 70 75 80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346  
 Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His  
 85 90 95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394  
 Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn  
 100 105 110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg 442  
 Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro  
 115 120 125 130

cag att gtg cag gct gtg tct tca gca cca gca ctt gaa act gac tct 490  
 Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser  
 135 140 145

tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca 538  
 Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser  
 150 155 160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc 586  
 Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser  
 165 170 175

gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct 634  
 49/735



295

300

305

ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa 1018

Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu

310

315

320

agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg 1060

Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu

325

330

335

tagagactgc atcaaccoga cattcctttc ttataccaat gtgaaatttc cagatcatct 1120

gtaaacctac aactttaata gaagactact aataacagaa gacaaattag tgaagaaaag 1180

acggagtttc gaaattgaat ggcagggtgg tttttgctta caagccattt ctgttcattc 1240

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gcatatactt gatagaaacc ataaagttgt agcagttaag tccagtcaca tttggttaat 1360

cagtgtttga tataattgaa agagttgagt ggataaacag tcttccagct tgtaaagcc 1420

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tgatatattac attattatctt aggaaaactc ttctgtgaaa taaccatgca taacttactt 1660







Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn  
245 250 255

Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu  
260 265 270

Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr  
275 280 285

Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu  
290 295 300

Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met  
305 310 315 320

Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu  
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<210> 20

<211> 2636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53)..(1060)

<400> 20



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 Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro  
 115 120 125 130

cag att gtg cag gct gcg tct tca gca cca gca ctt gaa act gac tct 490  
 Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser  
 135 140 145

tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca 538  
 Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser  
 150 155 160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc 586  
 Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser  
 165 170 175

gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct 634  
 Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala  
 180 185 190

gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag 682  
 Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu  
 195 200 205 210

gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga 730  
 Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg

215	220	225	
gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att			778
Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile			
230	235	240	
ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata			826
Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile			
245	250	255	
gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa			874
Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys			
260	265	270	
tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat			922
Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn			
275	280	285	290
gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt			970
Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu			
295	300	305	
ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa			1018
Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu			
310	315	320	
agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg			1060
Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu			
325	330	335	

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gtaaacctac aactttaata gaagactact aataacagaa gacaaattag tgaagaaaag 1180

acggagtttc gaaattgaat ggcagggtgg tttttgctta caagccattt ctgttcattc 1240

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accaaagtgc ctttataaga aaaataaatt ttgttttaag ggacatacca gttttaggga 1900





&lt;400&gt; 22

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cggcctccgc ggtgcctgcc ttcgctctca ggttgaggag ctcaagcttg ggaaa atg 178

Met

1

gtg tgc att cct lgi atc gtc att cca gtt ctg ctc tgg atc tac aaa 226

Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr Lys

5

10

15

aaa ttc ctg gag cca tat ata tac cct ctg gtt tcc ccc ttc gtt agt 274

Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val Ser

20

25

30

cgt ata tgg cct aag aaa gca ata caa gaa tcc aat gat aca aac aaa 322

Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn Lys

35

40

45

ggc aaa gta aac ttt aag ggt gca gac atg aat gga tta cca aca aaa 370

Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr Lys

50

55

60

65

gga cca aca gaa atc tgt gat aaa aag aaa gac taaagaaatt ttcctaaagg 423

Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp

70

75

accccatcat ttaaaaaatg gacctgataa tatgaagcat cttccttgta attgtctctg 483

acctttttat ctgagaccgg aattcaggat aggagtctag atatttacct gatactaate 543

aggaaatata tgatatccgt atttaaaatg tagttagtta tatttaatga cctcattcct 603

aagttccttt ttcgttaatg tagctttcat ttctgttatt gctgtttgaa taatatgatt 663

aatagaagg tttgtgccag tagacattat gttactaaat cagcacttta aaatctttgg 723

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gatagggaac aggggggaaac ttctttgaaa aatgaaacat ctgttacatt aatgtctaatt 1023

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tt 1085

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<211> 84

<212> PRT

<213> Homo sapiens

<400> 23

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Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val

20 25 30

Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile

35 40 45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr Trp

50 55 60

Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His Ser

65 70 75 80

Leu Ser Gly Leu

<210> 24

<211> 1593

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (65).. (316)







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Thr Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln		
	85	90 95
Leu Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met		
	100	105 110
Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly		
	115	120 125
Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile		
	130	135 140
Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr		
	145	150 155 160
Phe Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala		
	165	170 175
Leu Leu Phe		

<210> 26

<211> 1820





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Leu Phe

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gaatttcgta ttctttcatt ccactgtgta aagtgctaga cattttccaa tttaaaattt 820

tgctttttat cctggcactg gcaaaaagaa ctgtgaaagt gaatttattc agccgactgc 880

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atggctttcc cagaagacac tctggagacc ttgctggcag tgctagccag gaaacagagt 1300

gaccaaggga caagaaggga cttgcctaaa gccaccacgc aactcagcag cagaaccaag 1360

atgggccccca ggctcctcca tatggcccag ggcttaccac cctatcacac gtggccttgt 1420

ctagaccacg tcctgagcag gggagaggct cttgagacct gatgccctcc taccacatg 1480



50	55	60	
Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe			
65	70	75	80
Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val			
	85	90	95
Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp			
	100	105	110
Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe			
	115	120	125
Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His			
	130	135	140
His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro			
145	150	155	160
Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val			
	165	170	175
Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln			
	180	185	190
Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln			
	195	200	205





ctc ttc ctc ttc tcc aag ttc att gag ctg atg gac aca gtg atc ttt 502  
 Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe  
 115 120 125

att ctc cga aag aaa gac ggg cag gtg acc ttc cta cat gtc ttc cat 550  
 Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His  
 130 135 140

cac tct gtg ctt ccc tgg agc tgg tgg tgg ggg gta aag att gcc ccg 598  
 His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro  
 145 150 155 160

gga gga atg ggc tct ttc cat gcc atg ata aac tct tcc gtg cat gtc 646  
 Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val  
 165 170 175

ata atg tac ctg tac tac gga tta tct gcc ttt ggc cct gtg gca caa 694  
 Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln  
 180 185 190

ccc tac ctt tgg tgg aaa aag cac atg aca gcc att cag ctg atc cag 742  
 Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln  
 195 200 205

ttt gtc ctg gtc tca ctg cac atc tcc cag tac tac ttt atg tcc agc 790  
 Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser  
 210 215 220

tgt aac tac cag tac cca gtc att att cac ctc atc tgg atg tat ggc 838







Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys Phe  
 10 15 20 25

acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt ccg 267  
 Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg Pro  
 30 35 40

gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat cct 315  
 Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr Pro  
 45 50 55

cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag ggc 363  
 Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln Gly  
 60 65 70

tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac cca 411  
 Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr Pro  
 75 80 85

atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg gcc 459  
 Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro Ala  
 90 95 100 105

tac cac gag acc ctg gct gga gga gca gcc gcg ccc tac ccc gcc agc 507  
 Tyr His Glu Thr Leu Ala Gly Gly Ala Ala Ala Pro Tyr Pro Ala Ser  
 110 115 120

cag cct cct tac aac ccg gcc tac atg gat gcc ccg aag gcg gcc ctc 555  
 Gln Pro Pro Tyr Asn Pro Ala Tyr Met Asp Ala Pro Lys Ala Ala Leu  
 80/735























1 5 10 15  
Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp  
20 25 30  
Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe  
35 40 45  
Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly  
50 55 60  
Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys  
65 70 75 80  
Val Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr  
85 90 95  
Phe Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe  
100 105 110  
Ser Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly  
115 120 125  
Asp Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu  
130 135 140  
Gln Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu  
145 150 155 160





































































































































































































































































































































































































































































































































































































































































































































































































































































































































































































































































































































































































































































































































